REMARKS

The drawings have been amended in response to the Examiner's statement in the Notice to File Missing Parts of Nonprovisional Application ("Notice") mailed December 22, 2003. The Examiner stated in the Notice that the drawings contained excessive text and that although suitable descriptive legends may be used or required where necessary for an understanding of the drawing, they should contain as few words as possible. 37 CFR § 1.84(o). In response, the Applicants have amended Figures 1A, 1B, 4A, and 4B to comply with the drawing requirements under 37 CFR § 1.84.

Applicants believe that the present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

Respectfully submitted,

Date May 20, 2004 By _____

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Should additional fees be necessary in connection with the filing of this paper, or if a petition for extension of time is required for timely acceptance of same, the Commissioner is hereby authorized to charge Deposit Account No. 08-1641for any such fees; and applicant(s) hereby petition for any needed extension of time.

Title: CHIMERIC, HUMAN AND HUMANIZED ANTI-GRANULOCYTE ANTIBODIES AND METHODS OF USE
Inventor(s): GOLDENBERG et al.
Atty. Dkt. No.: 018733-1267

Annotated Marked-Up Drawings

Figure 1A shows the DNA sequence encoding MN3Vk cloned by RT-PCR and the predicted amino acid sequence. Underlined arrows indicate the PCR primer sequences. The putative CDR regions are in bold and underlined, and indicated. Nucleotide residues are numbered sequentially (right side). Kabat's Ig molecule numbering is used for amino acid residues (top of the residues).

Annotated Marked-Up Drawings

```
CAGGTCCAACTGCAGGAGTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATATCCTGCAAGGCTTCTGGGTATACCTTCAGA
---------+---------+---------+---------+---------+---------+---------+---------+---------+   90
GTCCAGGTTGACGTCCTCAGACCTGGACTCGACTTCTTCGGACCTCTCTGTCAGTTCTATAGGACGTTCCGAAGACCCATATGGAAGTCT
 1                 10                  20                  30
 Q  V  Q  L  Q  E  S  G  P  E  L  K  K  P  G  E  T  V  K  I  S  C  K  A  S  G  Y  T  F  R

AACTATGGAATGAACTGGGTGAAACAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATAT
---------+---------+---------+---------+---------+---------+---------+---------+---------+   180
TTGATACCTTACTTGACCCACTTTGTCCGAGGTCCTTTCCCAAATTTCACCTACCCGACCTATTTGTGGATGTGACCTCTCGGTTGTATA
                   40                  50       52A
 N  Y  G  M  N  W  V  K  Q  A  P  G  K  G  L  K  W  M  G  W  I  N  T  Y  T  G  E  P  T  Y
    CDR1                                                                          CDR 2

GCTGATGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTGCAGATCAACAACGTCAAAAATGAGGAC
---------+---------+---------+---------+---------+---------+---------+---------+---------+   270
CGACTACTGAAGTTCCCTGCCAAACGGAAGAGAAACCTTTGGAGACGGTCGTGACGGATAAACGTCTAGTTGTTGCAGTTTTTACTCCTG
60                 70                  80    82A B  C
 A  D  D  F  K  G  R  F  A  F  S  L  E  T  S  A  S  T  A  Y  L  Q  I  N  N  V  K  N  E  D

ACGGCTACATATTTCTGTGCAAGAAAGGGATGGATGGATTTCAACGGTAGTAGCCTCGACTACTGGGGCCAAGGGACCACGGTCACCGTC
---------+---------+---------+---------+---------+---------+---------+---------+---------+   360
TGCCGATGTATAAAGACACGTTCTTTCCCTACCTACCTAAAGTTGCCATCATCGGAGCTGATGACCCCGGTTCCCTGGTGCCAGTGGCAG
          90                   100 A  B  C  D  E                             110
 T  A  T  Y  F  C  A  R  K  G  W  M  D  F  N  G  S  S  L  D  Y  W  G  Q  G  T  T  V  T  V
                                  CDR3

TCCTCA
------
AGGAGT                                                                                       366
   113
 S  S
```

Figure 1B ~~shows the DNA sequence encoding MN3VH cloned by RT-PCR and the predicted amino acid sequence. Underlined arrows indicate the PCR primer sequences. The putative CDR regions are in bold and underlined, and indicated. Nucleotide residues are numbered sequentially (right side). Kabat's Ig molecule numbering is used for amino acid residues (top of the residues).~~

Annotated Marked-Up Drawings

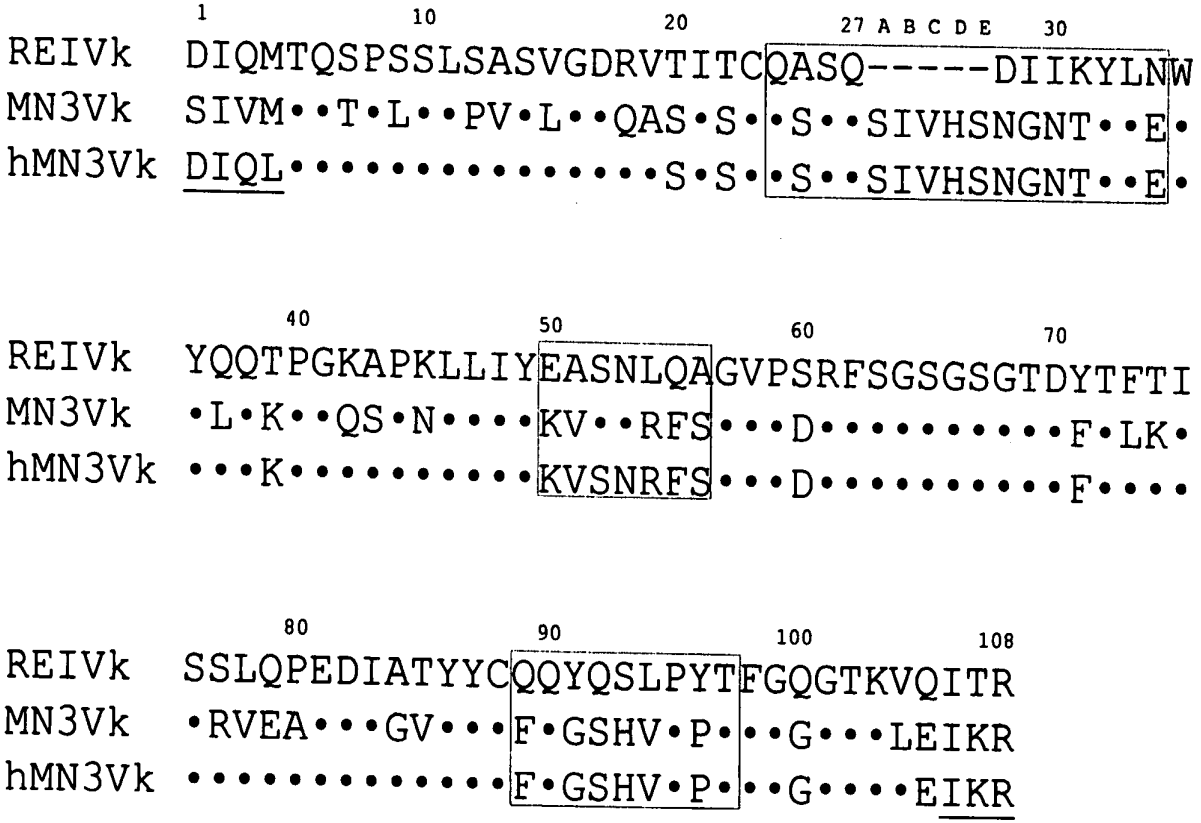

Figure 4A. Amino acid sequence alignment of REI, MN3 and hMN3 light chain variable domains. Dots indicate the residues in MN3 is identical to the corresponding residues in REI. Dashes represent gaps introduced to aid the alignment. Boxed represent the CDR regions. Both N- and C-terminal residues (underlined) of hMN3 are fixed by the staging vector used. Therefore, the corresponding terminal residues of MN3 are not compared with that of REI. Kabat's Ig molecule numbering scheme is used (same as in Fig. 1A).

Annotated Marked-Up Drawings

```
                1                   10                  20                  30                  40
EU_VH     PVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQA
MN3VH     QVQLQE••P•L••••ET••I••••••Y••RNYGMN••K••
hMN3VH    QVQLQ•••••••••••••••••••Y••RNYGMN••••

                          50  52 A            60                  70
EU_VH     PGQGLEWMGGIVPMFGPPNYAQKFQGRVTITADESTNTAY
MN3VH     ••K••K•••W•NTYT•E•T••DD•K••FAFSLET•AS•••
hMN3VH    •••••••••W•NTYT•E•T••DD•K••FAF•••••••••

                80  82 A B C            90                  100 A B C D E       110
EU_VH     MELSSLRSEDTAFYFCAGGYGIYS-----PEEYNGGLVTV
MN3VH     LQINNVKN•••T•••RKGWMDFNGSSLDY
hMN3VH    •••••••••••••••RKGWMDFNGSSLDY

                103         110  113
KOL_VH    WGQGTPVTVSS
MN3VH     •••••T•TVSS
hMN3VH    •••••••TVSS
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Figure4B. Amino acid sequence alignment of EU (FR1-3) and KOL (FR4), MN3 and hMN3 heavy chain variable domains. Dots indicate the residues in MN3 is identical to the corresponding residues in REI. Dashes represent gaps introduced to aid the alignment. Boxed represent the CDR regions. Both N- and C-terminal residues (underlined) of hMN3 are fixed by the staging vector used. Therefore, the corresponding terminal residues of MN3 are not compared with that of human VH sequences. Kabat's Ig molecule numbering scheme is used (same as in Fig. 1A).